

033034-0364-033034

GGACATAATCTGTGGGAGCAGT'TTATTCCAGTATCACCCAGGGTGCAGCCACCCAGGACTGT
GTTGAAGGGTGT'TTTTCTTTTAAATGTAACTACCTCTCATCT'TTCTTCTTACACAGT
TCTGAGAACGATTACATTATAGATAAGTAGTACATGGTGGTAACCTCTACT'TT'TTAGGAGGA
CTACTCTCTTCTGACAGTCTGACTGGTCTTCTACACTAAGACACCCATGAAGGAGTATGTG
CTCCTATTATTCTCGGCT'TGTGCTCTGCGAAACCCCTTCTTAGCCCTTGACAGTACGCACT
GAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATG
ATGATGATGATGAGGACAACTCTCT'TTTTCCAACAAGAGAGCAAGAAGCCATT'TTTTCC
TTTGATCTGTTTCCAATGTGTCCATTGGATGTCAGTGCTATTACAGAGT'TGTACATTGCT
AGAT'TTAGGTT'GACCTCAGTCCCAACCAACAT'TCCATT'TTGATATCGCAATGCTTGATCTCT
AAACAACT'AAAA'TAAGAAACTCAAAGAAATGAT'TTAAAGACTCACTTCATCT'TATGGT
CTGATCTCTGAACAACAACGAAGCTAACGAAGATTACCCAAAAGCC'TTCTAACCCAAAGAA
GTTGCGAAGGCTGTATCTGTCCCAACAACTAAGTGAAGTAACCACTTAATCTTCTCCAAAT
CATTAGCAGGACTCAGAAT'TCATGAATAAAGTTAAGAAATACAAAGGACACAT'CAAA
GGAATGAATGCTTTTACAGTT'TTGAAATGAGTGCAAACCCCTTGATATAATGGGATAGA
GCCAGGGGCATT'TGAAGGGGTGACCGTGTTCATATCAGAATTGCAGAAGCAAAACTGACCT
CAGT'TGCT'AAAGGCT'TACCACCAACT'TTATGGAGCTTCACTTGATTTATAATAAAAT'TTCA
ACAGTGGCAATCTGAGGAT'TTAAACGATACAAAGAACTCAAAGAGCTGGGCCTAGGAACA
CAAAATCACAGATATCGAAAAATGGGAGTCTTGCTAACATACACAGTGTGAGAGAATAACATT
TGAAAAACAATAAACT'AAAAAAATCCCTTCAGGAT'TACAGAGTGAAGTAACCTCGAGATA
ATCTTCTCTTAATCTTAATCAAT'TGCAAGAGTGGGAGTAATGACTTCTGTGCCAAGCTGCC
AAAGATGAAGAAATCTTTATACAGTGAATAAGT'TTATTCACAACCCCGTGAATACTGGG
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GGAATGTAATAAATTAGTAAT'TGGTAATGTCAT'TTAATAAGAT'TCAAAATCCCTACAT
TTGGAATCTTGAACCTCTAATTAATGTTAGTAT'TATATACAAAGAAATATCTATTCTCA
AGTGTGAAGTCCAAGTATTAAT'TTATGACAAGAAAT'TCAACGGAAT'TTGTGCCAAACTATT
GATACATAAGGGGTGAGAGAAACAAGCATCTATTGTGAGT'TTCTTTTGGGTACAAATGAT
CTTACATAAACTCATGCTTGACATTCTTTTCTTATAACAAAAAGTAAGATATTCGGTA
TTTAAACACTT'TGTATCAAGCATT'TTAAAAAGAACTGTACTGTAATGGAATGCTTGACT
TAGCAAAAAT'TGTGCTCTTTCATTGCTGT'TTGAAAAACAGAAATTAACAAGACAGTAAATG
GAAGAGTGCAATACACTATTCTTATCTTGTAGTAATCTGGGTAGTACTGTAATTTTAAAT
CATCTTAAAGTATGATTTGATATAATCTTATTGAAAT'TACCTTATCATGTCTTAGAGCCCGT
CTTTATGTTTAAAACTAATTTCTTAAAAATAAAGCCTCAGTAAATGTTCTATTACCAACTTGA
TAAATGCTACTATAAGAGCTGGT'TTGGGGCTATAGCATGTCTTTT'TTTT'TTAAATAT
ACCTGATTTAAAAATCTCTGTGAAAAACGTGTAGTGT'TTATAAAATCTGTAACCTCGCATTTT
AATGATCCCGCTATTATTAAGCT'TT'TTAATAGCATGAAAAATGTTTAGGCTATATAACATTGCCA
TTCAACTCTTAAGGAATATTTTGGATATATCCCTTTTGGAAAGCCTTGCTTGGAAAGAGCCTGGA
CACTAACAACTCTACACAAATGTGCTTTCAAATACGTATGGAAGTGGAATAACTCTGAGAAA
CACATCTAGTATAACTGAATAAGCAGAGCATCAAATTAACAGACAGAAACCGGAAGCTCTA
TATAAAAGTCTCAGAGTCTCTTATGTTATTTCTTATTTGGCATTCACATATGTAATAATCAGAAA
ACAGGGAAATTTTTCATTAATAAATATGGTTTCAAT

FIGURE 2

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392

<subunit 1 of 1, 379 aa, 1 stop

<MW: 43302, pI: 7.30, NX(S/T): 1

MKEYVLLFLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDNSLFPTREPR
SHFFPFDLFPMCPFGQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL
TSLYGLILNNNKLTKIHPKAFLT TTKLRRLYL SHNQLSEIPLNLPKSLAELRIHENKVKKIQ
KDTFGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLD
YNKISTVELED FKRYKELQRLGLGNNKITDIENGLANI PRVREIHLENNK LKKIPSGLP
KYLQIIFLHSNSIARVGVNDFCPTVPKMKKS LYS AISLFNNPVKYWEMQPATFRCVLSRMSV
QLGNFGM

Signal sequence.

amino acids 1-15

N-glycosylation site.

amino acids 281-285

N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

Leucine zipper pattern.

amino acids 154-176

100580" + 1932+202

FIGURE 3

CGGACGCGTGGGCGGACGCGTGGGCCGCCGACCGCCCCGGCCCGGCCCTCCGCCCTCCGCACTCGCGCCTCC
 CTCCCCTCCGCGCGCTCCCGCGCCTCTCCTCCTCCTCCCAGCTGTCCCGTTCCGGTCAATGCGAGCCTCC
 GGCCCCGCGGCCCGCTGTCTGTCTCCTCGGGCTGTCTGTCTCGGCTCCCGGCCGCCGCCGCGGCCCGCAGA
 GCCCCCGCTGTCTGCCATCCGTTCTGAGAAGGAGCGCGTCCCGTTTCGGGGAGCGCGAGGCTGCACCTTCGCGCG
 GAAGTCTATGCGCTTGGACGAGCTGGCACCCGGACCTAGGGCAGCCATTTCGGGTGATGCGCTGCTGTG
 CGCTTCGCGAGGCGCTCAGTGGGGTGGCGTACCGAGGGCCCTGGCAGGCTCAGCTGCAAGAAACATCAAAACAGA
 GTGCCAAACCCCCCTGTGGGCAGCGCGCCAGCTGCCGGACACTGCTGCCGAGACTGCCCCAGGAGCGCAG
 CAGTTCGGAGCGCGCAGCGGCGGCTGTCTTCAGGATATCCGCGGACCCGAGATCGCAGTTATAGCGACCG
 CGGGAGCCAGGCGCTGAGGAGCGGGCCCGTGTGACGGGCACACGGACTTCGTGGCGCTGCTGACAGGGCGAG
 GTCGCGAGGCGTGGCACGAGCCGAGTCTCGCTGCTGCGCTCTAGCCTCCGCTTCTCTATCTCTACAGGCGGCT
 GGACCGCCCTACAGGATCGCTTCTCAGACTCCAATGGCAGTGTCTGTTCAGACCCCTGCAGCCCCACCCA
 AGATGGCCTGGTCTGTGGGTGTGGCGGCGAGTGCCTCGGTTGTCTCTGCGGCTCCTTAGGGCAGAACAGCTGCA
 TGTGGCACTTGTGACACTCACTCACCTCTCAGGGGAGGTCTGGGGCCCTCTCATCCGCGACCGGCCCTGGCTGC
 AGAGACCTTCAGTGCCATCTGACTCTAGAAGGCCCCCCACAGCAGGGGCGTAGGGGGCATCACCTTGCTCACTCT
 CAGTGACACAGAGGACTCCTTGCACTTTTGTGCTCTTCGAGGGCTGCTGGAACCCAGGAGTGGGGGACTAAC
 CCAAGTCTCCCTTGAGGCTCCAGATTCTACACAGGGGCGAGTACTGCGAGAACTCAGGCCAATGTCTCAGGCCA
 GGAACCGAGCTTGTGTGAGGTGTGCCCAACCTGACACTCCAGAGATGGACTGGCTGGTGTCTGGGGAGCTGCA
 GATGGCCCTGGAGTGGGACGACGAGCGAGGGCTGCGCATCAGTGGACACATTTGCTGCCAGGAAGACTGCGACGT
 CCTGCAAGGTGCTCTTTGTGGGCTGATGCCCTGATCCCACTCAGAGCGGCTGCTGCGGCTCAGCCAGCTGCAC
 GCTGTCAAGAAATGGCTCTGATGCTATCAGGTGCAAGGTGTAAGGACCAAGGACTGAGTGGTGGCCATGACACT
 GGAGACCAAGCCTCAGCGGAGGATCAGCGCACTGTCTGTGCCACATGGCTGGAATCCAGCCAGGAGGACACAC
 GGCGCTGGGTATCTGCCCTGGGCTGGGTGCCGAGGGGCTCATATGCTGTGCGAGAATGACTCTTCTGAACTGT
 GGGCACCAAGGACTTCCAGACGGAGAGCTTCGGGGGCGAGTGGCTGCCCTGCCCTACTGTGGGCATAGCGCCCG
 CCATGACACGCTGCCGCTGCCCTAGCAGGAGCCCTGGTGTACCCCTGTGAAGAGCCGAAGCAGCAGGGCAGCG
 CTGGCTTTCCTTGGATACCCACTGTCACTGCACATGAAGTGTCTGTGGTGGGCTTGGTGGCTCAGAAACAGG
 CACTGTCACTGCCCACTCTCTTGGGCTCCTGGAACGCCAGGGCTCGGGCGGCTGTGTAAGGGAATTCATGGCTC
 AGAGGCCAGGGTGTGGTGAAGGACTGGAGCCGGAACCTGTCGCGCACCTGGCAAAAGGCATGGCCCTCCCTGAT
 GATCACCACCAAGGCTAGCCCCAGAGGGGAGCTCCGAGGGCAGGTGCACATAGCCAAACCAATGTGAGGTTTGGCG
 ACTGCGCCTGGAGGCGGCCGGGGCGAGGGGGTGGCGGCGCTGGGGGCTCCGATACAGCCTCTGTCTGCGCGCG
 TGTGTGTGCTGGTCTCCCGGCCCTAGCGCCCCGCAAACTGTGTGTCTGGGCGGCCCGAGAGCCCCAACACATG
 CTTCTTCGAGGGGCGAGCGCCCCACGCGGCTCGTGGGCGCCCACTACGACCCGCTCTGTCACTCTGCAC
 TGTCCAGAGCAAGCGACTGTGTGACCCTGGTGGTGTGCCACCGGCTGCCACCCCGAGTGGCCACACCCGGTGCAGGCTCC
 CGACCACTGCTGCCCTGTTTGCCCTGAGAAACAAGATCTCAGAGACTTGGCAGGGCTGCCAAGGAGCGCGGACCC
 AGGAGAGGGCTGCTATTTTGATGGTGTGACCGGAGCTGGCGGCGAGCGGTAACGCGTGGCAACCCCGTTGTGCCCCC
 CTTTGGCTTAATTAAGTGTGCTGTCTGCACCTGCAAGGGGGGCACTGGAGAGGTGCACTGTGAGAAGGTGCAAGT
 TCCCGGCTGGCTGTGGCCACGCTGTGCGTGTCAACCCCAACCGACTGCTGCAAAACAGTGTCCAGTGGGTGGG
 GGCCCCACCCAGCTGGGGGACCCATGCAAGGCTGATGGGCCCCGGGGCTGCCGTTTGTGTGGGAGTGGTTCCC
 AGAGAGTCAAGCTGGCACCCCTCAGTGGCCCCCTTTTGGAGAGATGAGCTGTATCACTTGCAAGTGTGGGGCAGG
 GGTGCTCTCTGTAGAGCGGATGACTGTTCACTGCCACTGTCTGTGGCTGGGGAAGGAGAGTGCATGTCTTC
 CCGCTGCACGGCCCCACGGCGGCCCCAGAGACCAAGAAGTATCAGAGCTGGAGAAAGAAGCCGAAGGCTCTTA
GSGAGACCGAGAGCGGCCAAGTGACCAAGAGGATGGGGCTGAGCTGGGGAAGGGGTGGCATCGAGACCTCTT
 GCATTCTCTGTGGGAAGCCAGTGCCTTTTGTCTCTGTCTCTCTACTCCACCCCACTACCTCTGCCGAA
 CCACAGCTCCACAGGGGGAGAGGACAGCTGGGCCAGCGAGTACAGCACTCAAGTCTCTGCCCTGCCACCC
 TCGGCTCTGTCTGGAAGCCCAACCCCTTCTCTCTGTACATAAGTGTACATGCTTGTGTGGATTTTAAATTAT
 TCTTCACTCAGCACCAAGGGCCCCGCACTCCACTCTGTCTGCCCTGAGCTGAGCAGAGTCAATTATTGGAGAG
 TTTTGTATTATTAAAAACATTTCTTTTCAGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

09473664-103001

FIGURE 4

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pI: 8.21, NX(S/T): 5

MPSPAPPAPAPLLLLGLLLGSRPARGAGPEPPVLPPIRSEKEPLPVRGAAGCTFGGKVYALDE
TWHFDLGQPFVGMRCVLCACEAPQWGRRTRGPGRVSCKNIKPECPPTACGQPRQLPGHCQQT
CPQERSSSSERQPSGLSFEYPRDPEHRSYSDRGEPGAEEERARGDGTDFVALLTGPRSQAVAR
ARVSLRLRSSLRFSISYRRLDRPTRIRFSDSNGSVLFEHPAAPTQDGLVCGVWRAVPRLSRL
LRAEQLHVALVTLTHPSGEVWGPLIRHRALAAETFSAILTLEGPPQQGVGGITLLTSLDTE
SLHFLLLFRGLLEPRSGGLTQVPLRLQILHQQLLRELQANVSAQEPGFAEVLPNLTQEMD
WLVLGELQMALEWAGRPGLRISGHIAARKSCDVLQSVLCGADALIPVQTGAAGSASLTLLGN
GSLIYQVQVVGTSSEVVAMTLETKPORRDQRTVLCHMAGLQPGGHTAVGICPGLGARGAHL
LQNELFLNVGTDKDFPDGELRGHVAALPYCGHSARHDTLPVPLAGALVLPVVKSSQAAGHAWLS
LDTHCHLHYEVLLAGLGSEQGTVTAHLLGPPGTPGPFRLLKGFYGSEAQGVVKDLEPELLR
HLAKGMASLMITTKGSPRGELRGQVHIANQCEVGGRLLEAAGAEGVRALGAPDTASAAPPVV
PGLPALAPAKPGGPGRPDRDNTCCFFEGQQRPHGARWAPNYDPLCSLCTCQRRTVICDPVVP
PPSCPHPVQAPDQCCVPCPEKQDVRDLPLGLPRSRDPGEGCYFDGDRSWRAAGTRWHHPVVPF
GLIKCAVCTCKGGTGEVHCEKVQCPRLACAQPVVRNPTDCKQCPVSGAHPQLGDPMQADG
PRGCRFAGQWPFESQSWHPVSPVPPFGEMSCITCRCGAGVPHCERDDCSLPLSCSGSGKESRCS
RCTAHRPPETRTDPELKEAEGS

Signal sequence.

amino acids 1-23

N-glycosylation sites.

amino acids 217-221, 351-355, 365-369, 434-438

Tyrosine kinase phosphorylation sites.

amino acids 145-153, 778-786

N-myristoylation sites.

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242,
390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579,
576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877,
905-911

Amidation site.

amino acids 87-91

Cell attachment sequence.

amino acids 165-168

Leucine zipper pattern.

amino acids 315-337

100220-19269

FIGURE 5

GCGGAGCAGCCCTAGCCGCCACCGTCTGCTCTCGCAGCTCTCGTCCCACTGCCACCGCCGCGCGCTCACTGCG
 TCTGGGTTCGGGTCCCGCGCCCTCCCGCGCGCC**ATG**CAGCCCCCGCGCGCCAGCGCCCGGTGCGCAGCTCG
 TGCCCCGCGCTGCGCCTGCTGCTGCTGCTGCTCGGAGCGGGGCCCGCAGGCGAGCTCCCTGGCCAAACCCGGTGCCCG
 CCGCGCCCTTGCTGCGCCCGGGCCGTGCGCCGCGCAGCCCTGCCGAATGGGGGTGTGTGCACCTTCGCGCCCTG
 AGCCGGACCCGACGACCCCGGCCCGCCCGCGCGAGCCTGGCTACAGCTGCACCTGCCCGCCGGGATCTCCGGCG
 CCAACTGCCAGCTTGTTCAGATCCTTGTGCCAGCAACCTTGTCCACATGCGCAACTGCACGACGACGACGACGAC
 CGACGACGATGTGCTTACCTCTGCAATTGCAATGAAGGCTATGAAGTCCCAACTGTGAACAGGCACTTCCAGCTG
 TCCAGGCCACTGGCTGGACCGAATCATGGCACCCCGACAGCTCAGCCTGTTCTGTGCTCTCAGGAGCCTCTG
 AAATCCTGCCTCGCTCTCAGGCAACGGTGACACTGCTACTTGGCAGCCGAAACAGGGCAGAAAGTTGTAGAAA
 TGAATGGGATCAAGTGGAGGTGATCCAGATATTGCTGTGGGAATGCCAGTTCTAACAGCTCTCGCGGTGGCC
 GCCTGGTATCCTTTGAAGTGCCACAGAACCTCAGTCAAGATTCCGGCAAGATGCCACTGCTCTCAGTATTGTG
 TCTGGAAGGTACGCGCCACAGGATCCAAACAGTGCTCCTCATAGATGGCAGAAAGTGTGACCCCCCTTCAGGCTG
 CAGGGGAGCTGGTCTCTCGTGGAGAGATGCTCGCTTGGGGAATAATCACTTTATTTGGTTTTGTGAATGATCTG
 TGACTAAGTCTATTGTGGCTTTCGGCTTAACTCTGGTGGTGAAGGTACAGACCTGTGTGCGCGGGGAGAGTCAG
 CAAATGACTTGGAGTGTTCAGGAAAAGGAAAATGCACCAGAAAGCGCTCAGAGGCAACTTTTCTGTACTCTGTG
 AGGAGCAGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGGCAGAGGAAACCTTGCCAAACACACGCGAGCT
 GTATTGATGCAAAATGAAGCAAGATGGGAGCAATTTCACTGTGTTTTGCTTCTCGTTTACTGGAGAGCTTT
 GCCAGTCCAAGATTGATTACTGCACTCTAGACCCATGAGAAATGGAGCAACATGCATTTCCAGTCTCAGTGGAT
 TCACCTGCGCAAGTGTCCAGAGGATACCTCGGATCTGCTTGTGAAGAAAAGGTGGACCCCTGCGCCTCGCTCCGT
 GCCAGAACACCGCACCTGCTATGTGGACGGGTACACTTTACCTGCAACTGTGAGCCCGGCTTCACAGGCGCGA
 CCTGTGCCAGCTTATTGACTTCTGTGCCCTCAGCCCCCTGTGCTCATGGCAGCTGCCCGAGCGTGGGCACAGCT
 ACAAAATGCTCTGTGATCCAGGTTTACCATGGCCTCTACTGTGAGGAGAAATATAATGAGTGCCCTTCCGCTCCAT
 GCCTGAATGCAGCCACTGACAGGACCTCGTTAATGGCTATGAGTGTGTGTGCTTGGCAGAAATACAAAGGAACAC
 ACTGTGAATTGTACAAGGATCCCTGCGCTAACGTCAGCTGTCTGAACGGAGCCACTGTGACAGCGACGCGCTGA
 ATGGCCAGTGCATCTGTGACCCCGGGTTTACAGGTGAAGAGTGCAGACATTGACATAAATGATGTGACAGTAAAC
 CTGCGCACCATGTGTGGGAGTGCTCGGACAGGCCAATGGTTATAACTGCCACTGCCCGCATGGTGGTGGGAG
 CAAACTGTGAGATCCACCTCCAATGGAAGTCCGGGCACATGGCGGAGAGCTCACCAACATGCCACGGCACTCCC
 TCTACATCATCATTGGAGCCCTCTGCGTGGCCTTCATCCTTATGCTGATCATCTGATCGTGGGGATTTCGCGCA
 TCAGCCGCATTGAATACCAAGGTTCTTCCAGGCCAGCCTATGAGGAGTTCTACAACCTGCCCGAGCATCGACAGCG
 AGTTGCAAGATGCCATTGCATCCATCCGGCATGCCAGGTTTGGAAAGAAATCCCGGCCCTGCAATGTATGATGTGA
 GCCCATCGCCTATGAAGATTACAGTCTTGATGACAAACCTTGGTCACTGATTAAAACTAAAGATTGT**TAAT**
 CTTTTTTGGATTATTTTTCAAAGATGAGATACTACACTCATTAAATATTTTTAAGAAATATAAAGCTTAA
 GAAATTTAAATGCTAGCTGCTCAAGAGTTTTCACTAGAATATTTAAGAACTAAATTTCTGCAGCTTTTAGTTTG
 GAAAAAATTTTAAAAACAAATTTGTGAACCTATAGACGATGTTTTAATGTACCTTCAGCTCTCTAAACTGT
 GTGCTTCTACTAGTGTGTGCTCTTTCACTGTAGACACTATCACGAGACCAGCTTAATTTCTGTGGTGTGTACA
 GAATCAAGTCTAACTCAAGGAAGTTTTCTGTTGACGTTTGAGTGCCGCTTCTGAGTAGAGTTAGGAAAAACAC
 GTAACGTAGCATATGATGTATAATAGAGTATACCCGTACTTAAAGAAAGTCTGAATGTTCGTTTTGTGGAAA
 AGAAACTAGTTAAATTTACTATTCTAACCCGAATGAAATAGCCTTTGCTTATTCTGTGCATGGGTAAAGTAAC
 TATTCTGCACTGTTTGTGTAACCTTGTGGAACACTTCTTCAGTTGTTTTGTCATTTCGTGAACAGGTG
 TCGAATCAGGCCCTCAAAACATACGTAAACGAAAGGCCCTAGCGAGGCAAAATCTGATTGATTGTAATCTATATTT
 TTCCTTAAAGTACAGGGTTCTATATTGTGAGTAAATTAATTTACATTTGAGTTGTTTTGTTGCTTGAAGAGGTAG
 TAAATGTGAAGAGTACTGGTCTCTCAGTAGTGAGTATTCTCATAGTGCAGCTTATTATTATCTCCAGGATGTT
 TTTGTGCTGTATTGAATTGATATGTGCTTCTTCTGATTCTTGCTAATTTCCAACCATATTGAATAAATGTGATC
 AAGTCA

09473664.037001

FIGURE 6

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQPRRAQAPGAQLLPALALLLLLLLGGAGPRGSSSLANVPVPAAPLSAPGPCAAQPCRNGGVCTSR
PEPDQHPAPAGEPGYSCTCPAGISGANCLVADPCASNPCHHGNCSSSSSSSDGYLCICN
EGYEGPNCEQALPSLPATGWTESMAPRQLQVPVATQEPDKILPRSQATVTLPTWQPKTGQKV
VEMKWDQVEVIPDIACGNASSNSAGRLVSFEVPQNTSVKIRQDATASLILLWKVTATGFGQ
QCSLIDGRSVTPLQASGGVLVLEEMLALGNNHFIGFVNDSVTKSIVALRLTLVVKVSTCVPG
ESHANDLECSGKGKCTTKPSEATFSCCTCEEQYVGTFCEEYDACQRKPCQNNASCIDANEKQD
GSNFTCVCLPGYTGLCQSKIDYCILDPGRNGATCISLSSGFTQCCEGYFGSACEEKVDPC
ASSPCQNNGTQCYVDGVHFTCNCSFGFTGPTCAQLIDFCALSPCAHGTCRSVGTSYKCLCDPG
YHGLYCEEYNECLSAFCLNAATCRDLVNGYECVCLAELYKGTCHCELYKDPKANVSCLNGATC
DSDGLNGTCICAPGFTGEEDIDINECDSPNCHHGGSCLDQPNGYNCHCPHGWVGANCEIHL
QWKSGHMAESLTNMPRHSLYIIIGALCVAFILMLIILIVGICRISRIEYQGSSRPAYEEFYN
CRSIDSEFSNAIASIRHARFGKKSPPAMYDVSPDIAYEDYSPDDKPLVTLIKTKDL

Signal sequence.

amino acids 1-28

Transmembrane domain.

amino acids 641-660

N-glycosylation sites.

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,
375-379, 442-446, 549-553, 564-568

Glycosaminoglycan attachment site.

amino acids 320-324

Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

N-myristoylation sites.

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,
373-379, 449-455, 480-486, 562-568, 565-571

Amidation site.

amino acids 702-706

Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

EGF-like domain cysteine pattern signatures.

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,
491-503, 529-541, 567-579, 605-617

09942664.063001

FIGURE 7

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTTCAGGCTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA
ATCACTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACT
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTC
AGGAAAAGGAAAATGCACCACGAAGCCGTGAGAGGCAACTTTTTCCTGTACCTGTGAGGAGC
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCC
TGTTTATACTGGAGAGCTTTGCCAACCGAAC TGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

09943664.033001

FIGURE 8

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAAGTGTGA
CCCCCCTTTCAGGCCTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA
ATCACTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACT
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTC
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCCTGTACCTGTGAGGAGC
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTCACCTGTGTTTGCCTTCC
TGGTTTACTGGAGAGCTTTGCCAACCGAACCTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

09942664.063001

FIGURE 9

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAG
GCCCCCAGAGCCCTCACCACGCTGGGCGCCCCAGAGCCCACACCATGCCGGGCACCTAC
GCTCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGCCCT
GATGCGGGACTTCCCGCTCGTGGACGGCCACAACGACCTGCCCTGGTCTTAAGGCAGGTTT
ACCAGAAAGGGCTACAGGATGTTAACCTGCGCAATTTCAGCTACGGCCAGACCAGCCTGGAC
AGGCTTAGAGATGGCCTCGTGGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCA
GGACCGGGATGCCCTGCGCCTCACCTTGGAGCAGATTGACCTCATACGCCGATGTGTGCCT
CCTATTCTGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCC
TGCTCATCGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTT
CTACATGTCTGGGAGTGCCTACCTGACGCTCACCCACACCTGCAACACACCCTGGGCAGAGA
GCTCCGCTAAGGGCGTCCACTCCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGAG
AAGGTGGTGGCAGAAATGAACCGCCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGC
TGTGGCACGGCGGGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCCACTCGGTGCC
GGGTGTGTGCAACAGTGTCTCGGAATGTTCTGTGATGACATCCTGCAGCTTCTGAAGAAGAAC
GGTGGCGTCGTGATGGTGTCTTTGTCCATGGGAGTAATACAGTGCAACCCATCAGCCAATGT
GTCCACTGTGGCAGATCACTTCGACCACATCAAGGCTGTCTATGGATCCAAGTTTCATCGGGA
TTGGTGGAGATTATGATGGGGCCGGCAAATTCCTCAGGGGCTGGAAGACGTGTCCACATAC
CCGGTCTCTGATAGAGGAGTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTT
TCGTGGAACCTGCTGCGGTCTTTCAGACAAGTGGAAAAGGTACAGGAAGAAAACAAATGGC
AAAGCCCCCTGGAGGACAAGTTCGCGGATGAGCAGCTGAGCAGTTCTGCCACTCCGACCTC
TCACGTCTGCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACCTCACTGAGATTCCCATACA
CTGGACAGCCAAGTTACCAGCCAAGTGGTCAGTCTCAGAGTCCTCCCCCACATGGCCCCAG
TCCTTGCAAGTTGTGGCCACCTTCCAGTCCTTATTCTGTGGCTCTGATGACCCAGTTAGTCC
TGCCAGATGTCACTGTAGCAAGCCACAGACCCCCACAAAGTTCCCCTGTGTGTCAGGCACA
AATATTTCTGAAATAAATGTTTTGGACATAG

0942664-08301

FIGURE 10

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595
<subunit 1 of 1, 433 aa, 1 stop
<MW: 47787, pI: 6.11, NX(S/T): 5
MPGTYAPSTTLSSPSTQGLQEALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSGLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIIRMCASYSELELVTSAKALND
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVS DAVARRALEV SQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPVLIIEELLSRGWSEBELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPVLAVVATFPVLILWL
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N-glycosylation sites.

amino acids 58-62, 123-127, 182-186, 273-277

N-myristoylation sites.

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

Renal dipeptidase active site.

amino acids 134-157

FIGURE 11

AAAACTATAAATATTCCGGATTATTCATACCGTCCCACCATCGGGCGCGGATCCGCGGCCG
CGAATTCTAAACCAACATGCCGGGCACCTACGCTCCCTCGACCACACTCAGTAGTCCCAGCA
CCCAGGGCCTGCAAGAGCAGGCACGGGCCCTGATGCGGGACTTCCCGCTCGTGGACGGCCAC
AACGACCTGCCCTTGGTCTTAAGGCAGGTTTACCAGAAAGGGCTACAGGATGTTAACTTGC
CAATTTCACTACGGCCAGACAGCCTGGACAGGCTTAGAGATGGCCTCGTGGGCGCCAGT
TCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCGGGATGCCCTGCGCCTACCTGGAG
CAGATTGACCTCATACGCCGATGTGTGCCTCCTATTCTGAGCTGGAGCTTGTGACCTCGGC
TAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCCTCATCGGTGTAGAGGGTGGCCACTCGC
TGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCTGGGAGTGCCTACCTGACGCTC
ACCCACACCTGCAACACACCCTGGGCAGAGAGCTCCGCTAAGGGCGTCCACTCCTTCTACAA
CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGCAGAAATGAACCGCCTGGGCA
TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGGCCCTGGAAGTGTACAG
GCACCTGTGATCTTCTCCCACTCGGCTGCCCGGGTGTGTGCAACAGTGCTCGGAATGTTCC
TGATGACATCCTGCAGCTTCTGAAGAAGAACGGTGGCGTGTGATGGTGTCTTTGTCCATGG
GAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGATCACTTCGACCACATC
AAGGCTGTCATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGATGGGGCCGGCAAATT
CCCTCAGGGGCTGGAAGACGTGTCCACATACCCGGTCTGATAGAGGAGTTGCTGAGTCGTG
GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTTCGTGGAAACCTGCTGCGGGTCTTCAGACAA
GTGGAAAAGGTACAGGAAGAAAACAAATGGCAAAGCCCTTGGAGGACAAGTTCCCGGATGA
GCAGCTGAGCAGTTCTTGCCACTCCGACCTCTCACGTCTGCGTCAGAGACAGAGTCTGACTT
CAGGCCAGGAACCTCACTGAGATTCCCATACACTGGACAGCCAAGTTACCAGCCAAGTGGTCA
GTCTCAGAGTCTTCCCCCACCCTGACAAAACCTCACATGCCCAACCGTGCCAGCACCTGA
ACTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACACC

FIGURE 12

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872
><subunit 1 of 1, 446 aa, 0 stop
><NX(S/T): 5
MPGTYAPSTTLSSPSTQGLQEQARALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTS�DRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIRMCASYSELELVTSAKALND
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNGGVVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKPPQGLE
DVSTYPVLIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPKWSVSESSPHDPKTHTCPPCPAPELLGGP
SVFLFPPKPKDT
```

091364 03201

FIGURE 13

CGCCAGCGAGTGGCGGGCGGCTGGCCCGCGCCCTCCCGCGCCCGGCTGCGTCCCGCGCC
 CTGCGCCACCGCCGCCGAGCCGACGCCCGCGCGCCCGCGGAGCGCGGCCCCATGCCC
 GCCGGCCGCCGGGGCCCCGCCGCCCAATCCGCGCGCGCGCCGCCCGCTTGCTGCCCCCTGCT
 GCTGCTGCTCTGCGTCTCTCGGGCGCGCGAGCCGGATCAGGAGCCACACAGCTGTGATCA
 GTCCCCAGGATCCACGCTTCTCATCGGCTCCTCCCTGCTGGCCACCTGCTCAGTGACCGGA
 GACCCACAGGAGCCACCGCCGAGGGCTCTACTGGACCTCAACGGGCGCGCCCTGCCCCC
 TGAGCTCTCCCGTGTACTCAACGCCTCCACCTTGGCTCTGGCCCTGGCCAACCTCAATGGGT
 CCAGGCAGCGGTGGGGGACAACTCGTGTGCCACGCCGTGACGGCAGCATCCTGGCTGGC
 TCCTGCCCTCTATGTTGGCTGCCCGCAGAGAAACCGTCAACATCAGTGTGTTCCAAAGAA
 CATGAAGGACTTGACCTGCGGCTGGACGCCAGGGGCCACGGGGAGACCTTCTCCACACCA
 ACTACTCCCTCAAGTACAAGCTTAGGTGGTATGGCCAGGACAACACATGTGAGGAGTACCAC
 ACAGTGGGGCCCCACTCCTGCCACATCCCAAGGACCTGGCTCTCTTTACGCCCTATGAGAT
 CTGGGTGGAGGCCACCAACCGCCTGGGCTCTGCCGCTCCGATGTACTACGCTGGATATCC
 TGGATGTGGTGACCACGACCCCCGCCCGACGTGCACGTGAGCCGCTGGGGGCTGGAG
 GACCAGCTGAGCGTGCCTGGGTGTCGCCACCGCCCTCAAGGATTTCTCTTTCAAGCCAA
 ATACCAGATCCGCTACCGAGTGGAGGACAGTGTGGACTGGAAGTGGTGGACGATGTGAGCA
 ACCAGACCTCCTGCCGCTGGCCGGCCTGAAACCCGGCACCGTGTACTTCGTGCAAGTGCGC
 TGCACCCCTTTGGCATCTATGGCTCCAAGAAAGCCGGGATCTGGAGTGAGTGGAGCCACCC
 CACAGCCGCTCCACTCCCGCAGTGAGCGCCCGGGCCCGGGCGCGGGGCGTGCGAACCGC
 GGGCGGAGAGCCGAGCTCGGGGCCGGTGCGGCGGAGCTCAAGCAGTTCTTGGGCTGGCTC
 AAGAAGCACGCGTACTGTCCAACCTCAGCTTCCGCCTCTACGACCAGTGGCGAGCTGGAT
 GCAGAAGTCGCACAAGACCCGCAACCAGGACGAGGGGATCCTGCCTCGGGCAGACGGGGCA
 CGGCGAGAGGTCTTCCAGATTAAGCTGTAGGGGCTCAGGCCACCTCCTGCCACGTGGAGA
 CGCAGAGGCCGAACCCAACTGGGGCCACCTCTGTACCCTCACTTCAGGGCACCTGAGCCAC
 CCTCAGCAGGAGCTGGGGTGGCCCTGAGCTCCAACGGCCATAACAGCTCTGACTCCCACGT
 GAGGCCACTTTGGGTGCACCCAGTGGGTGTGTGTGTGTGAGGGTTGGTTGAGTTGC
 CTAGAACCCCTGCCAGGGCTGGGGGTGAGAAGGGGAGTCATTACTCCCCATTACCTAGGGCC
 CCTCCAAAAGAGTCCTTTTAAATAAATGAGCTATTTAGGTGCTGTGATGTGAAAAA
 AACAAAAAAAAAAAAA

0993664.03301

FIGURE 14

><ss.DNA38113

><subunit 1 of 1, 422 aa, 1 stop

><MW: 46302, pI: 9.42, NX(S/T): 6

MPAGRRGPAQAQSARRPPPLPLLLLLCVLGAPRAGSGAHTAVIS PQDPTLLIGSSILLATCSV
HGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSIL
AGSCLYVGLPPEKPVNISCSKNMKDLTCRWTPGAHGETFLHTNYS LKYKLRWYGQDNTCEE
YHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTPPPDVHVS RVGG
LEDQLSVRWVSFPALKDFLFQAKYQIRYRVESVDWKVVDDVSNQTSCLAGLKPGTVYFVQ
VRCNPFGIYGSKKAGIWEWSHPTAASTPRSERPGPGGGACEPRGGEPSSGFPVRRELKQFLG
WLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGPAR

Signal sequence.

amino acids 1-30

Transmembrane domain.

amino acids 44-61

N-glycosylation sites.

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 413-417

N-myristoylation sites.

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

Amidation site.

amino acids 3-7, 79-83, 411-415

Growth factor and cytokines receptors family signature 2.

amino acids 325-331

00173661.032001

0904-687X

[illegible]

FIGURE 16

```
</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436
<subunit 1 of 1, 300 aa, 1 stop
<MW: 32964, pI: 9.52, NX(S/T): 1
MKFLLDILLLLPLLVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQ
```

Signal sequence.

amino acids 1-19

Transmembrane domain.

amino acids 170-187

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 30-34, 283-287

N-myristoylation sites.

amino acids 43-49, 72-78, 122-128, 210-216

0047664.00001

FIGURE 17

GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAGCGGAGCCGGCAGGGAGCGAACCAGGACTG
 GGGTGACGGCAGGGCAGGGGGCGCCTGGCCGGGGAGAAGCGCGGGGGCTGGAGCACCACCAA
 CTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACT
 GCGAGAGGACCCCGCGTCCGGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCCTGC
 TGCTCCTGGGCCTGGCGGCCGGCTCGCCCCACTGGACGACAACAAGATCCCCAGCCTCTGC
 CCGGGGCACCCCGCCTTCCAGGCACGCGGGGCCACCATGGCAGCCAGGGCTTGCCGGGGCG
 CGATGGCCGCGACGCGCGCAGCGCGCGCCCGGGGCTCCGGGAGAGAAAGGCGAGGCGGGGA
 GGCCGGGACTGCCGGGACCTCGAGGGGACCCCGGGCGCGAGGAGAGGCGGGACCCCGGGGG
 CCCACCGGCCTGCCGGGGAGTGCTCGGTGCCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTC
 CGAGAGCCGGGTGCCCTCCGCCGTCTGACGCACCCCTTGCCCTTCGACCGCGTGCTGGTGAACG
 AGCAGGGACATTACGACGCCGTACCCGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTAC
 TTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGA
 ATCCATTGCCCTCTTCTTCCAGTTTTTCGGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGGG
 GGGCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTTGGGTGCAGGTGGGTGTGGGTGACTAC
 ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTTCTCCGATTTCTGGTGTACTCCGA
 CTGGCACAGCTCCCCAGTCTTTGCTTAGTGCCCACTGCAAAGTGAGCTCATGCTCTCACTCC
 TAGAAGGAGGGTGTGAGGCTGACAACCAGGTATCCAGGAGGGCTGGCCCCCTTGGAAATATT
 GTGAATGACTAGGGAGGTGGGGTAGAGCACTCTCCGCTCTGCTGTGGCAAGGAATGGGAAC
 AGTGGCTGTCTGCGATCAGGTCTGGCAGCATGGGGCAGTGGCTGGATTCTGCCCCAAGACCA
 GAGGAGTGTGCTGTGCTGGCAAGTGAAGTCCCCAGTTGCTCTGGTCCAGGAGCCCCACGGT
 GGGGTGCTCTCTCTGGTCTCTGCTTCTCTGGATCCTCCCCACCCCTCCTGCTCCTGGG
 GCCGGCCCTTTTCTCAGAGATCACTCAATAAACCTAAGAACCCTCATAAAAAAAAAAAAAA
 AAAAAAAAAAAAAA

0942664-033001

05943164-08-001

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><subunit 1 of 1, 243 aa, 1 stop
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MRPLLVLVLLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPRDGRDGRDGAPGAP
GEKGEGGRPGLPGRGDPGRGEAGPAGTGPAGECSVPPRSAFSAKRSES RVPPSPDAFLP
FDRVLVNEQGHYDAVTGKFTCQVPGVYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWP
KPAASGGAMVRLEPEDOVWVOVGVDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA

amino acids 1-15

amino acids 11-17, 68-74, 216-222

amino acids 77-80

FIGURE 19

CTCTTTTGTCCACCAGCCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG
AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCAACAGACCAT
GCTGCATCCAGAGACCTCCCCTGCGCGGGGCATCTCTGGCTGTGCTCCTGGCCCTCCTTG
GCACCACCTGGGCAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC
CTGAACAGGAAGGAGAGTTTCTTGCTCCTCTCCCTGCACAACCGCCTGCGCAGCTGGGTCCA
GCCCTTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCACTGGCTCAAG
CCAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCTTG
CAAGTGGGCTGGAACATGCAGCTGCTGCCGCGGGCTTGGCGTCCTTTGTGAAGTGGTCAG
CCTATGTTTTCAGAGGGGCAGCGGTACAGCCACGCGGCAGGAGAGTGTGCTCGCAACGCCA
CCTGCACCCACTACACGCAGCTCGTGTGGGCCACCTCAAGCCAGCTGGGCTGTGGGCGGCAC
CTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGTGCCTACTCCCCGGAGGCCAA
CTGGGAGGTCAACGGGAAGACAATCATCCCCATAAGAAGGGTGCCTGGTGTTTCGCTCTGCA
CAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATGCAGGGGGCTCTGTGAGGTCCCC
AGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGACGCTCTAACATCAGCACCTGCCACTG
CCACTGTCCCCCTGGCTACACGGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTGC
ACGGCCGGTTCGGGAGGAGGAGTGTCTGTCGCTCTGTGACATCGGCTACGGGGGAGCCGAG
TGTGCCACCAAGGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTT
CATGGTGTCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTGAGGAAAGGCG
GGGTGCTGGCCAGATCAAGAGCCAGAAAGTGCAGGACATCCTCGCCTCTATCTGGGCCGC
CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACCTCTGGATCGGCT
CACCTACAAGACCGCCAAGGACTCCTTCGCTGGGCCACAGGGGAGCACCAGGCCCTCACCA
GTTTTGCTTTTGGGCAGCCTGACAACCACGGGCTGGTGTGGCTGAGTGTGCCATGGGTTT
GGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTTCAACTGGAACGACAGCGCTGCAAAAC
CCGAAACCGTTACATCTGCCAGTTTGCCAGGAGCACATCTCCCGTGGGGCCAGGGTCTCT
GAGGCCTGACCACATGGCTCCCTCGCCTGCCCTGGGAGCACCGGCTCTGCTTACCTGTCTGC
CCACCTGTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAAGAGGTCTCAGA
CCTTGACAATGCCAGAAGTTGGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTG
AGTGTTAGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGA
TGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAAGGCTGCTCTCTTCCACCTGGCCCAGAC
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CTGAAAAAAAAAAAAA

09973664.03201

FIGURE 20

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176
<subunit 1 of 1, 455 aa, 1 stop
<MW: 50478, pI: 8.44, NX(S/T): 2
MLHPETSPGRSHLLAVLLALLGTTWAEVWPPQLQEAPMAGALNRKESFLLLSLHNRLRSWV
QPAAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVV
SLWFAEQQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCAGQTAIEAFVCAYSPGG
NWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPRMSCQNHGRNLNISTCH
CHCPPGYTGRYQVRCSLQCVHGRFEEBECSCVCDIGYGGAGCATKVHFPFHTCDLRIDGDC
FMVSSEADTYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLTTNEVTDSDFETRNFWIG
LTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCK
TRNRYICQFAQEHISRWGPGS

Signal sequence.

amino acids 1-26

Transmembrane domain.

amino acids 110-124

N-glycosylation sites.

amino acids 144-148, 243-247

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 45-49

N-myristoylation sites.

amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,
288-294, 331-337, 398-404

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 204-215

EGF-like domain cysteine pattern signature.

amino acids 249-261, 280-292

C-type lectin domain signature.

amino acids 417-442

097364+032001

FIGURE 21

CGGACGCGTGGGCTGGGCGCTGCAAAGCGTGTCCCGCCGGGTCCCCGAGCGTCCCGCGCCCT
CGCCCGCC**ATG**CTCCTGCTGCTGGGGCTGTGCCCTGGGGCTGTCCCTGTGTGTGGGGTCGCA
GGAAGAGGCGCAGAGCTGGGGCCACTCTTCGGAGCAGGATGGACTCAGGGTCCCGAGGCCAAG
TCAGACTGTTGCAGAGGCTGAAAACCAAACCTTTGATGACAGAATTCTCAGTGAAGTCTACC
ATCATTTCCCGTTATGCCCTTCACTACGGTTTCCTGCAGAATGCTGAACAGAGCTTCTGAAGA
CCAGGACATTGAGTTCCAGATGCAGATCCAGCTGCAGCTTTCATCACCACTTCACTATGC
TTATTGGAGACAAGGTGTATCAGGGCGAAATTACAGAGAGAGAAAAAGAGTGGTGATAGG
GTAAAAAGAGAAAAGGAATAAAACCAGAGAAGAAAATGGAGAGAAGGGGACTGAAATATTAG
AGCTTCTGCAGTGATTCCCGAGCAAGGACAAAGCCGCCCTTTTCCTGAGTTATGAGGAGCTTC
TGCAGAGGCGCTTGGGCAAGTACGAGCACAGCATCAGCGTGGCGCCCCAGCAGCTGTCCGGG
AGGCTGAGCGTGGACGTGAATATCCTGGAGAGCGCGGGCATCGCATCCCTGGAGGTGCTGCC
GCTTCACAACAGCAGGCGAGAGGGGCGAGTGGGCGCGGGGAAGATGATTCTGGGCCTCCCCCAT
CTACTGTCTATTAACCAAAATGAACACATTTGCCAACATAATTTTAAACCTACTGTAGTACAA
CAAGCCAGGATTGCCCAGAATGGAATTTTGGGAGACTTTATCATTAGATATGACGTCAATAG
AGAACAGAGCATTTGGGGACATCCAGGTTCTAAATGGCTATTTTGTGCACTACTTTGCTCCTA
AAGACCTTCCCTTTACCAAGAATGTGGTATTCTGTGCTTGACAGCAGTGCTTCTATGGTG
GGAACCAAACTCCGGCAGACCAAGGATGCCCTCTTCACAATTCTCCATGACCTCCGACCCCA
GGACCGTTTTCAGTATCATTTGGATTTCACACCGGATCAAAGTATGGAAGGACCACCTTGATAT
CAGTCACTCCAGACAGCATCAGGGATGGGAAAGTGATACATTACCATATGTCAACCATGGA
GGCACAGACATCAACGGGGCCCTGCAGAGGGCCATCAGGCTCTCAACAAGTACGTGGGCCCA
CAGTGGCATTGGAGACCGGAGCGTGTCCCTCATCGTCTTCTGACGGGATGGGAAGGCCACGG
TCGGGGAGACGCACACCTCAAGATCCTCAACAACACCCGAGAGGCGCCCCGAGGCCAAGTC
TGCATCTTACCATTGGCATCGGCAACGACGTGGACTTCAGGCTGTGGAGAACTGTCCCT
GGAGAAGCTGTGGCCTCACACGGCGCGTGCAGAGGAGGAGGACGCAAGCTCGCAGGTCATCG
GGTCTACGATGAAATCAGGACCCCGCTCCTCTCTGACATCCGCATCGATTATCCCCCAGC
TCAGTGGTGCAGGCCACCAAGACCTGTTCCCAACCTACTTCAACGGCTCGGAGATCATCAT
TGCGGGGAAGCTGGTGGACAGGAAGCTGGATCACCTGCACGTGGAGGTACCGCCAGCAACA
GTAAGAAATTCATCATCTGAAGACAGATGTGCCCTGTGCGGCCTCAGAAGGCAGGGAAAGAT
GTCACAGGAAGCCCCAGGCCTGGAGGCGATGGAGAGGGGGACCAACCACATCGAGCGTCT
CTGGAGCTACCTCACCAAAAGGAGCTGTCTGAGCTCCTGGCTGCAAAAGTGACGATGAACCGG
AGAAGGAGCGGCTGCGGCAGCGGGCCAGGCCCTGGCTGTGAGCTACCGCTTCCTCACTCCC
TTCACCTCCATGAAGCTGAGGGGGCCGGTCCCACGCATGGATGGCCCTGGAGGAGGGCCACGG
CATGTCCGCTGCCATGGGACCCGAACCGGTGGTGCAGAGCGTGCAGGAGCTGGCAGCCGAGC
CAGGACCTTTGCTCAAGAAAGCCAAACTCCGTCAAAAAAAACAAAAACAAAAAAGAGA
CATGGGAGAGATGGTGTTTTTCTCTCCACCACCTGGGGATACGATGAAGAAATGGCCACCT
GCAAGCCAGGAAGACGGCCCTCACCAGACACCATGTCTGTGCGACCTTGATCTTGGACCTC
CCAGCCTCCAGAACTGTGAGAAATAAATGTGTTTTGTTAAGCTAAAAAAGAAAAAAGAAAA
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0913664-083001

0543434 : 0543434

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<subunit 1 of 1, 694 aa, 1 stop

<MW: 77400, pI: 9.54, NX(S/T): 6

MLLLLGLCLGLSLCVGSGQEEAQSWGHSSEQDGLRVPRQVRLQLRKTPLMTEFSVKSTIIS
 RYAFTTVSCRMNLRASEQDIEFQMQUIPAAAFITNFTMLIGDKVYQGEITEREKKSGDRVKE
 KRNKTEENGEKGTEIFRASAVIPSKDKAAFFLSYEELLQRRLGKYEHSISVRPQQLSGRLS
 VDVNILESAGIASLEVPLPHNSRQRGSGRGEDDGGPPPTVINQNETFANIIFKPTVVQQA
 IAQNGILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVFVFLDSSASVMGTK
 LRQTKDALFTILHDLRPQDRFSIIGFSNRKVKWDHLISVTPDSIRDGVYIHHMSPTGGTD
 INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTGDKPTVGETHTLKLINNTREAAARGQVCIF
 TIGIGNDVDFRLLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV
 QATKTLFPNYFNGSEIIAGKLVDRKLDHLHVEVTASNSKKFIILKTDVVRPQKAGKDV
 SPRPGGDGEGDTNHIERLWSYLTTEKELSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTS
 MKLRGPVPRMDGLEEAHGMSAAMGPEPVVQSVRGAGTQPGPLLKKPNSVKKKQNKTKRHGR
 DGVFPLHHLGIR

Signal sequence.

amino acids 1-14

N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

FIGURE 23

CGGACGCGTGGGGTGCCCGACATGGCGAGTGTAGTGCTGCCGAGCGGATCCCAGTGTGCGGC
GGCAGCGGCGGCGGCGGCGCTCCCGGGCTCCGGCTTCTGCTGTTGCTCTTCTCCGCCCGCG
CACTGATCCCCACAGTGTATGGGCAGAATCTGTTTACGAAAGACGTGACAGTGTATCGAGGGA
GAGGTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTACGCTACTGAA
TCCCAACAGGCAGACCATTTTATTTTTCAGGGACTTCAGGCCCTTTGAAGGACAGCAGGTTTCAGT
TGCTGAATTTTCTAGCAGTGAACCTCAAAGTATCATTGACAAACGTCTCAATTTCTGATGAA
GGAAGATACTTTTGCCAGCTCTATACCGATCCCCACAGGAAAGTTACACCACCATCACAGT
CCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG
AGATTGAAGTCAACTGCACTGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGGTTCAAA
GGGAACACAGAGCTAAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGAC
CAGTCAGCTGATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCCAGTGTATCGCCAGGTGG
AGCACCTGCGGTCACTGGAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT
CAAGTGACATTCAGATGACTTATCCTCTACAAGGCTTAACCCGGAAGGGGACGCGCTTGA
GTTAACATGTGAAGCCATCGGGAAGCCCCAGCCTGTGATGGTAACTTGGGTGAGAGTCGATG
ATGAAATGCCTCAACACGCCGTACTGTCTGGGCCCAACCTGTTCAATAACCTAAACAAA
ACAGATAATGGTACATACCGCTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTA
TATGCTGTATGTATACGATCCCCCACAACCTATCCCTCCTCCACAACAACCACCACCACCA
CCACCACCACCACCACCACCTCCTTACCATCATCAGAGTTCGCGAGCAGGTGAAGAAGGC
TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTCGTGGCGGTGGTGGTGTTCGCCAT
GCTGTGCTTGCTCATCTTCTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTC
ATGAAGCCAAAGGAGCCGATGACGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGA
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0997364.03301

FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518
<subunit 1 of 1, 440 aa, 1 stop
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QVNKSDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSELKVSLTNVSIISDEGRYFCQL
YTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKG
KSEVEEWSDMYTVTSQLMLKVHKEDDGVVPVICQVEHPAVTGNLQTRYLEVQYKQPQVHIQMT
YPLQGLTREGDALELTCEAIGKPPQPMVTVWRVDEMPQHAVLSGPNLFINNLNKTONGTYR
CEASNIVGKAHSDMYLVYDPPTTIPPTTTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDH
AVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEE
KKEYFI

Signal sequence.

amino acids 1-36

Transmembrane domain.

amino acids 372-393

N-glycosylation sites.

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,
430-434

Tyrosine kinase phosphorylation sites.

amino acids 233-240, 319-328

N-myristoylation sites.

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,
411-417, 427-433, 428-432

0943664.083001

FIGURE 25

GGGGGGGGTGGACGCGGACTCGAACGCAAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCCGA
 CCCGCCAGGAAAGACTGAGGCCGCGGCTGCCCGCCCGGCTCCCTGCGCCGCCGCCGCCCTC
 CCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCGCTGCTCCTCTGCTACTGGCCCT
 GGGGCTTGGGTGTCAGGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCT
 GCAGTGCCTGCCCGGAGGCCACCGTGCCTCCGAGACGTGCCACCCGACACGTTGGGGTGTAC
 GTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCGGCTGCGCGGCTGCA
 GCTCTGGACCTGTACAGAACAGATCGCCAGCCTGCGCCTGCCCGCCTGCTGCTGCTGG
 ACCTCAGCCACAACAGCCTCTGGCCCTGGAGCCCGGCATCTGGACACTGCCAACGTGGAG
 GCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGCTCTTCAGCCGCTTGGC
 CAACCTCCACGACCTGGATGTGTCCGACAACAGCTGGAGCGAGTGCCACCTGTGATCCGAG
 GCCTCCGGGGCTGACGCGCTGCGGCTGGCCGGCAACACCGCATTTGCCAGCTGCGGCC
 GAGGACCTGGCCGGCTGGCTGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGC
 CTGCTTGGCGACCTCTCGGGCCTCTCCCCCGCTGCGGCTGCGCAGCTGCCGCAACC
 CCTTCAACTGCGTGTGCCCTGAGCTGGTTTGGCCCTGGGTGCGCGAGAGCCACGTCA
 CTGGCCAGCCCTGAGGAGACCGCTGCCACTTCCCCGCCAAGAACGCTGGCCGGCTGCTCT
 GGAGCTTGACTACGCCGACTTTGGTGTGCCAGCCACCAACAGCCACCAAGTGTGCCACCA
 CGAGGCCGTGGTGGCGGAGGCCACAGCCTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGC
 CCCACAGCGCCGGCCACTGAGGCCCCAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCC
 TGTCCCCCAGCCCCAGGACTGCCACCCTCCACTGCTTCAATGGGGGACATGTCACCTGG
 GACACGCGCCACCACTTGGCCTGCTGTGTGCCCGAAGCTTACCGGCCCTGTACTGTGAGAGC
 CAGATGGGGCAGGGGACACGGCCAGCCCTACACCAAGTCAAGCCGAGGCCACCAACGCTCCCT
 GACCTGGGATCGAGCCGGTGGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCC
 AGGGGAGCTCCGTGCACTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT
 AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGTGTAGTACACGGTCAACCAAGCTGCG
 GCCAACCGCCACTTACTCCGTCTGTGTATGCTTGTGGGGCCGGGGCGGGTGGCCGAGGGG
 AGGAGGCTTCCGGGGAGGCCATACACCCCGAGCCGTCCACTCCAACCAAGCCCAAGTCAAC
 CAGGCCCGCGAGGGCAACCTGCCGCTCTCATTGCGCCCGCCTGGCCGCGGTGCTCCTGGC
 CGCGCTGGCTGCGGTGGGGGCGAGCTACTGTGTGCGCGGGGGCGGGCCATGGCAGCAGCG
 CTCAGGACAAAGGCGAGGTGGGGCCAGGGCTGGGCCCTGGAAGTGGAGGGGCTGGAAGGTC
 CCCTTGGAGCCAGGCCGGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGA
 GTGTGAGGTGCCACTCATGGGCTTCCAGGGCTGGCCCTCAGTCAACCCCTCCACGCAAGAC
 CCTACATCTAAAGCCAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGC
 CAGCCCTCCTGCTGCCACACCACTAAGTTCTCAGTCCCAACCTCGGGAGTGTGGCAGAG
 CAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCTCTGGACCTCGGTCTCTCATCTGTGAG
 ATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCCTATGAGGACAGTGT
 CGCCCTGCGCTCCGCAACGTGCAGTCCCTGGGACACGCGGGCCCTGCCATGTGCTGGTAAC
 GCATGCTGGGCCCTGCTGGGCTCTCCACTCCAGGCGGACCTGGGGGCCAGTGAAGGAAG
 CTCGCCGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGTGACTCTAGTCTTGGCCCCAGG
 AAGCGAAGGAACAAAAGAACTGGAAGGAAGATGCTTTAGGAACATGTTTGTCTTTTAA
 AATATATATATATTATAGAGAGATCCTTTCCATTATTTCTGGGAAGATGTTTTTCAAACTC
 AGAGACAAGGACTTTGGTTTTTGTAAAGCAACCATGATATGAAGGCCCTTTGTAAAGAAAA
 ATAAAAAAAAAA

09443664.083001

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, pI: 7.24, NX(S/T): 3

MCSRVPLLLLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTPRDPVPDTPVGLYVFEN
GITMLDASSFAGLPGLQLLDLSQNIASLRLPRLLLDLSDHNSLLALEPGILDANVEALRL
AGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDLA
GLAALQELDVSNLSLQALPGDLSGLFPRRLRLAAARNPFCVCPLSWFGPWWRESHVTLASP
EETRCHFPKKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAP
ATEAPSPSTAPPTVGPVPPQDCPPSTCLNGGTCCHLGRHHLACLCPGFTGLYCESQMGQ
GTRPSPTPVTPRPPRLTLGIEPVSPSTSLRVGLQRYLQGSVQLRSLRLTYRNLSPGDKRLV
TLRLPASLAEYTVTQLRPNATYSVCVMPGLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQARE
GNLPLLIAPALAAVLLAALAAVGAAYCVRGRAMAAAAQDKQVGPAGPLELEGVKVPLEP
GPKATEGGGEALPSGSECEVPLMGFPGPLQSPHAKPYI

Signal sequence.

amino acids 1-23

Transmembrane domain.

amino acids 501-522

N-glycosylation sites.

amino acids 198-202, 425-429, 453-457

Tyrosine kinase phosphorylation site.

amino acids 262-270

N-myristoylation sites.

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

EGF-like domain cysteine pattern signature.

amino acids 355-367

Leucine zipper pattern.

amino acids 122-144, 194-216

004366.083001

FIGURE 27

GGCACTAGGACAACCTTCTTCCCTTCTGCACCACTGCCCGTACCTTACCCGCCCCGCCACC
TCCTTGCTACCCCACTCTTGAAACCACAGCTGTTGGCAGGTCCTCCAGCTC**ATG**CCAGCCTC
ATCTCCTTCTCTTGCTAGCCCCCAAGGGCCTCCAGGCAACATGGGGGGCCAGTCAGAGAGC
CGGCACCTCTCAGTTGCCCTCTGGTTGAGTTGGGGGGCAGCTCTGGGGGCCGTGGCTTGTGCC
ATGGCTCTGCTGACCCAACAAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA
GGGGACAGGAGGCCCTCCCAGAATGGGAAGGGTATCCTTGGCAGAGTCTCCCGGAGCAGA
GTTCCGATGCCCTGGAAGCCTGGGAGAATGGGGAGAGATCCCGAAAAGGAGAGCAGTGCTC
ACCCAAAAACAGAAGAAGCAGCACTCTGTCTGCACCTGGTTCCTATTAAACGCCACCTCCAA
GGATGACTCCGATGTGACAGAGGTGATGTGGCAACCAGCTCTTAGGCGTGGGAGAGGCCTAC
AGGCCCAAGGATATGGTGTCCGAATCCAGGATGCTGGAGTTTATCTGCTGTATAGCCAGGTC
CTGTTTCAAGACGTGACTTTACCATGGGTGAGGTGGTGTCTCGAGAAGGCCAAGGAAGGCA
GGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCACCCGGACCGGGCCTACAACAGCT
GCTATAGCGCAGGTGTCTTCCATTTACACCAAGGGGATATTCTGAGTGTATATAATCCCCGG
GCAAGGGCGAACTTAACCTCTCTCCACATGGAACCTTCCTGGGTTTGTGAACTG**TG**ATT
GTGTTATAAAAAGTGGCTCCAGCTTGGAAGACCAGGGTGGGTACATACTGGAGACAGCCAA
GAGCTGAGTATATAAAGGAGAGGGAATGTGCAGGAACAGAGGCATCTTCTGGGTTTGGCTC
CCCGTTCCTCACTTTTCCCTTTTCATTCCCACCCCTAGACTTTGATTTTACGGATATCTTG
CTTCTGTTCCCCATGGAGCTCCG

0912664.063001

FIGURE 28

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52722

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27433, pI: 9.85, NX(S/T): 2

MPASSPFLAPKGGPPNMGGFVREPALSVALWLSWGAALGAVACAMALLTQQTELQSLRREV
SRLQGTGGPSQNGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTQKQKKQHSVLHLVPIN
ATSKDDSDVTEVMWQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREG
QGRQETLFR CIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARA KLNLSPHGTF LGFVKL

Signal sequence.

amino acids 1-40

N-glycosylation site.

amino acids 124-128

Tyrosine kinase phosphorylation site.

amino acids 156-164

N-myristoylation site.

amino acids 36-42, 40-46, 179-185, 242-248

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 34-45

0994364 063001
100280 1993+660

FIGURE 29

CACTTTCTCCCTCTCTTCTTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTTCGCAGAGAC
 CTCGGAGACCGCGCCGGGAGACGGAGGTGCTGTGGGTGGGGGGGACCTGTGGCTGCTCGTA
 CCGCCCCCACCCTCTCTTCTGCACCTGCCGTCTCCGGAAGACCTTTTCCCTTGCTCTGT
 TCCTTCACCGAGTCTGTGCATCGCCCCGACCTGGCCGGGAGGAGGCTTGGCCGGCGGGGAGA
 TGCTCTAGGGGCGGCGCGGGAGGAGCGGCCGCGGGACGCGAGGGCCCGGCAGGAAGATGGGC
 TCCCGTGGACAGGGACTCTTCTGGCGTACTGCCTGCTCCTTGCTTGGCTCTGGCTTGGT
 CCTGAGTCGTGTGCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC
 CGTCCCTCCGACCATGCCGAGAGGGGTGAAGAAACAACATGAAAAATACAGGCCCACTCAG
 GACCAGGGGCTCCCTGCTTCCCGGTGCTTGCCTGCTGTGACCCCGGTACCTCCATGTACCC
 GCGCAGCCCGTGCCCCAGATCAACATCACTATCTTGAAGGGGAGAGGGTGACCGCGGAG
 ATCAGAGGCTCCAAGGAAATATGGCAAAACAGGCTCAGCAGGGGCCAGGGGCCACACTGGA
 CCAAAGGGCAGAAGGGCTCATGGGGGCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGC
 CTTTTCGGTGGCGGGAAGAGCCCATGCACAGCAACCACTACTACCAGCGGTGATCTTCG
 ACACGGAGTTCTGTAACTCTACGACCACTTCAACATGTTACCCGGCAAGTTCTACTGCTAC
 GTGCCCGCCTCTACTTCTTCAAGCTCAACGTGCACACCTGGAACCAAGAGGAGACCTACCT
 GCACATCATGAAGAACGAGGAGGAGGTGGTGTCTTTCGCGCAGGTGGCGACCCGACGCA
 TCATGCAAAAGCCAGAGCTGATGCTGGAGCTGCGAGAGCAGGACCAAGGTGTGGGTACGCCCTC
 TACAAGGGCGAAGCTGAGAACGCCATCTTCAAGCGAGGAGCTGGACACCTACATCACCTTCA
 TGGCTACCTGGTCAAGCAGCCACCGAGGCCCTAGCTGGCCGGCCACCTCTTCTCTCTCGCC
 ACCTTCCACCCCTGCGCTGTGCTGACCCACCGCCTCTTCCCGATCCGTGGACTCCGACTC
 CCTGGCTTGGCATTCACTGAGACGCCCTGCACACAGAAAGCCAAAGCGATCGGTCTCC
 CAGATCCCGCAGCTCTGGAGGAGCTGACCGCAGATGAATACCAAGGGCGGGGACCCCGC
 GAGAACCTCTTGGGACCTTCCGCGGCCCTCTCTGCACATCTCAAGTACCCCGCAGCGC
 GAGACGCGGTTGGCGGCAGGGCGTCCAGGGTGCAGCACCGCGGCTCCAGTCTTGGAAATA
 ATTAGGCAAAATCTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGGAGGCAAGAAAGGG
 TTGTTATTTTGTCTTCCAGCCAGCCTGCTGGCTCCCAAGAGAGAGGCTCTTTCAGTTGAG
 ACTCTGCTTAAGAGAAGATCCAAAGTTAAAGCTTGGGGTCAAGGGGAGGGGCCGGGGCAGG
 AAACCTACCTCTGGCTTAATCTTTTAAAGCCAGTAGGAACCTTCTTGGAGGATAGGTGGACC
 CTGACATCCCTGTGGCCTTGGCCAAAGGGCTCTGCTGCTCTTCTGAGTCACAGTCGAGGT
 GATGGGGCTTGGGCCCCAGCGCTCAGCTCCCAAGGAGGACCTGAGCCCCCTGCTTGGC
 TCCAGGTTGGTAGAAGCAGCCGAAGGGCTCTGACAGTGGCCAGGGACCCCTGGGTCCCCA
 GGCCTGCAGATGTTCTATGAGGGGAGAGCTCCTTGGTACATCCATGTGTGGCTCTGCTCC
 ACCCTGTGCCAACCCAGAGCCCTGGGGGTGGTCTCCATGCTGCACCCCTGGCATCGGCT
 TTCTGTGCCGCTCCACACAAATCAGCCCCAGAAGGCCCGGGGCTTGGCTCTGTGTTTT
 TATAAAACACCTCAAGCAGCACTGAGTCTCCCATCTCTCTGTTGGCTAAGCATCACCGCT
 CCACGTGTGTGTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCAGTGCCT
 CATCCAGGCTCTGACAGTAGCCTGAGAGGGGCTTTTCTAGGCTTCAGAGCAGGGGAGAG
 CTGGAAGGGGCTAGAAAGCTCCCGTGTGTCTGTTCTCAGGCTCCTGTGAGCCTCAGTCTGT
 AGACAGAGGTCAGAGGAAGTACAGTCCCAATCACCCGTGTCAGGATCACTCTCAGGAGC
 TGGCTGGCAGTGGGCAATAGGCCCTGTGGCAATTGCAAGCCAGCTGGAGCAGGGTGTGG
 GTGTCTCCACGCTGCTCTGCCCTGCCCATGGCCACCCAGACTCTGATCTCCAGGAACCCC
 ATAGCCCCCTCCACCTCAGCCCATGTTGATGCCAGGGTCACTCTTGTACCCGCTGGGCC
 CCAAAACCCCGCTGCTCTCTTCTTCCCCCATCCCCACCTGGTTTGAATTAATCTGTC
 TTCCCTCTCTGGGCTGGCTGCCGGGATCTGGGGTCCCTAAGTCCCTCTCTTAAAGAACTT
 CTGCGGGTCAAGACTGTAAGCCGAGTTGCTGTGGCGTGCCCGAAGCAGAGCGCCACACTC
 GCTGCTTAAGCTCCCCAGCTCTTCCAGAAAACATTAAACTCAGAATTGTGTTTCAA

0941364-033001

FIGURE 30

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234
><subunit 1 of 1, 281 aa, 1 stop
><MW: 31743, pI: 6.83, NX(S/T): 1
MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEQHEKYRP
SQDQGLPASRCLRCCDPGTSMPATAVPQINITILKGEKGDGRGLQGKYGKTGSAGARGH
TGPKGQKGSMGAPGERCKSHYAAFSVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMFTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWV
RLYKGERENAIFSEELDTYITFSGYLVKHATEP
```

Signal sequence.

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

09473664 032001
100230 + 19031650

FIGURE 31

GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCGCGGGATTGCGCGGTCTTCCCGCGG
 GCGCGACAGAGCTGTCTCGCACCCTGGATGGCAGCAGGGGCGCCGGGTCTCTCGACGCCA
 GAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAATAAGACCAAGAGGGAGGATTAT
 CCTTGACCTTTGAAGACCAAACTAACTGAAATTTAAATGTTCTTGGGGGAGAAGGGAG
 CTTGACTTACACTTTGGTAATAATTTGCTTCTGACACTAAGGCTGTCTGCTAGTCAGAATT
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCAATGACATCCAGTCATCTTTCTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAAATTTGCTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACCTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCGACA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCAGGAAGATTCTCTTACATGGCCAATTTTACAAGCAGTCACCTCCCC
 TAGCCCATCATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTACAAATTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCCTGAAATGTGAGTGCCTCCAGCTACGGTGGCAGTTGCTTCTCCA
 CATACCACCTCGGCTACTCCAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACC
 TTCTGGGACTTCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC
 AGCCTCCCAGCACCCTCATTTCTACAGTTTACACGGGCTGCGGCTACACTCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
 AACCATAACGTTTACAGAAATCTCCAACCTAACTTTGAACACAGGGAATGTGTATAACCCCTA
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCCTGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTCTTCCAGGGCAGTGTCCAGAAAAATCAGTACGGCCTTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTGTTCTGCTGGTATAGGCC
 TCGTCTCTCGGTAGAAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTGGAT
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAATCGGTGTCTCTTAATTCATT
 TAGTAACCAAGCCCAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG
 TATTTTGAAGACAGGAAATGCCCCCTTCTGCTTCTCTTTTTTTTTTGGAGACAGAGTCTT
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGTCTC
 CTGGGTTCAAGCGATTCTCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACCTGGGTGATTTTGTATTTTATAGTAGAGACGGGGTTTCAACATGTTGGTCAGGCTG
 GTCTCAAACCTCTGACCTAGTGATCCACCCTCCTCGGCTCCCAAAGTGTGGGATTACAGG
 CATGAGCCACCACAGCTGGCCCCCTTCTGTTTATGTTTGGTTTTTGAAGGAATGAAGTG
 GGAACCAAATTAGTAATTTTGGGTAATCTGCTCTAAAATATTAGCTAAAAACAAGCTCT
 ATGTAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTCAACTGGCTTTTATGCAAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTTCTGGTTCAGATAAAATCAAC
 TGTTTATATCAATTTCAATGGATTGCTTTTCTTTTATATGATTGCTTTAAACCTATT
 CCAGATGTAGTTCCTTCCAATTAAATATTGAATAAATCTTTGTACTCAA

09943664-063001

FIGURE 32

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYTLVII CFLT LRLSASQNCLKKSL EDVVIDIQSSLSKGIRGNFVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPN CYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSL LHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASAQLLAYKEKGHSQSSQSFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP
TDSKGSLETIPTFEISNLTLTNGVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFPEKWL LIGSLLFGVLFVLVIGLVLLGRILSESLRRKRYSRLDYLINGIYVDI
```

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

09042604.033001

FIGURE 33

GCGGCACCTGGAAGATGCGCCCATTTGGCTGGTGGCCTGCTCAAGSTGGTGTTCTGGTCTTC
GCCTCCTTGTGTGCCTGGTATTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT
GTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCTCAAAGCTCCAGTCC
CCAAAAGGCAAAAATGTGACCACCTGGACTCCCTGCCCATCTGACACCTATGCCCTACAGGTTA
CTCAGCGAGGTGGCAGAAGCAAGTACGCCAAAAATCTGCTTTGAGGATAACCTACTTATGGG
AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAACCTGGGA
ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG
TTTATTACAGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACA
TGAAATTCAGGTCTAGCTGGGTATTTATTGCAGCAAAAAGGCTTGGAACCTCCCTCCGAAATT
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACAACAGATATTCTGGCTGGCCTGCAGA
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCTGACTGACACTGCAGGTCTCTGAGTAAAT
GTGTTCTGTATAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTCTAAATCCAACA
GCCCCATATTTGATGAGTATTTTGGGTTTGTGTAAACCAATGAACATTTGCTAGTTGTATCA
AATCTTGGTACGCAGTATTTTATACAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGA
AACTAAAATGAATGGAAATTTCTTAAAAAAAAA

0943664.03001

FIGURE 34

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777
><subunit 1 of 1, 235 aa, 1 stop
><MW: 25982, pI: 9.09, NX(S/T): 2
MRPLAGGLLKVVVFVFWFASLCWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT
RCFDMEYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCI PKERS
```

Signal sequence.

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125

2025-10-10 10:10:10